

Cyanogen Bromide (CNBr) Cleavage

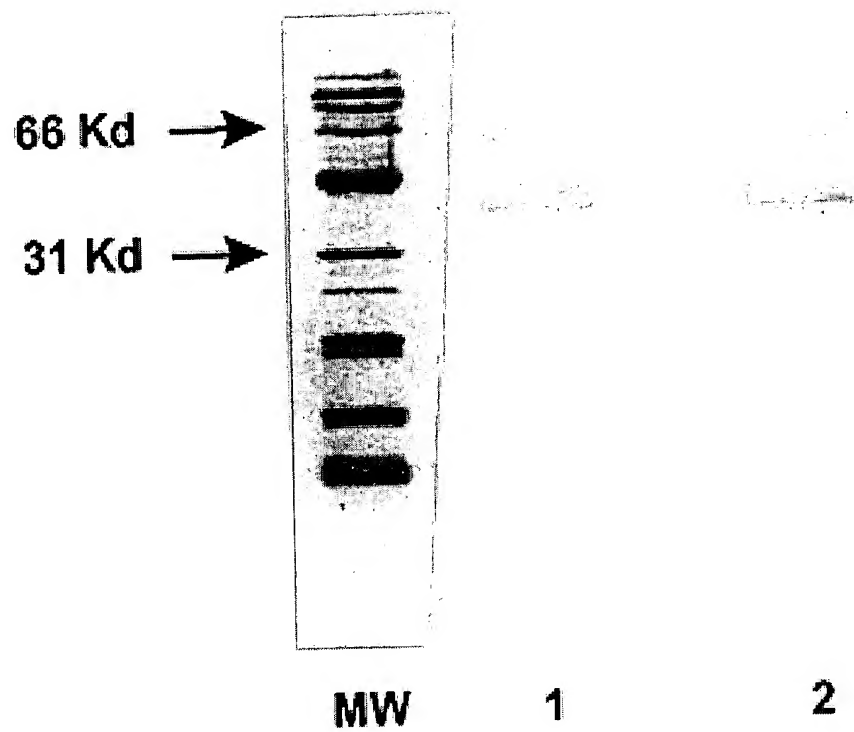


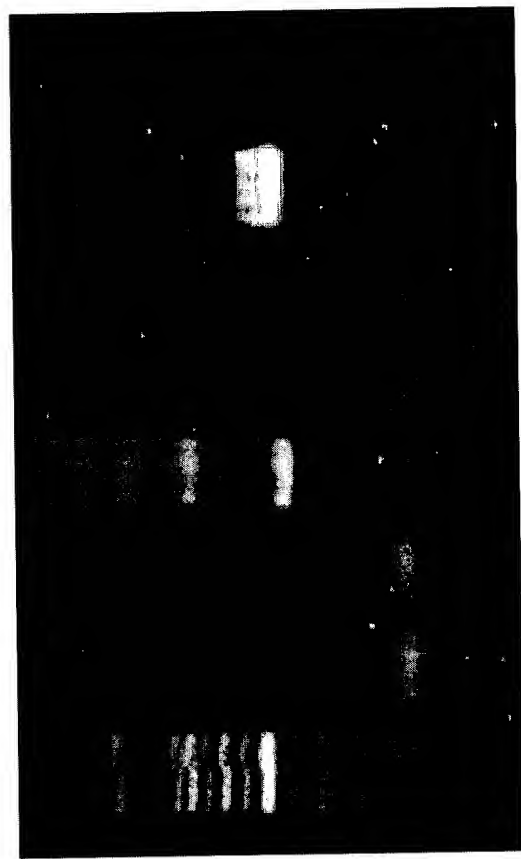
Figure 1

09955738.092704

TO2260" 82453660

A

1 2 3 4 5 6



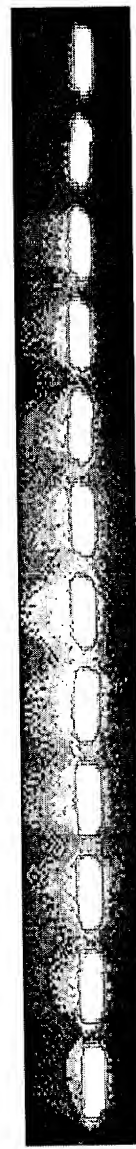
500 bases

B

1 2 3 4 5 6 7 8 9 10 11 12



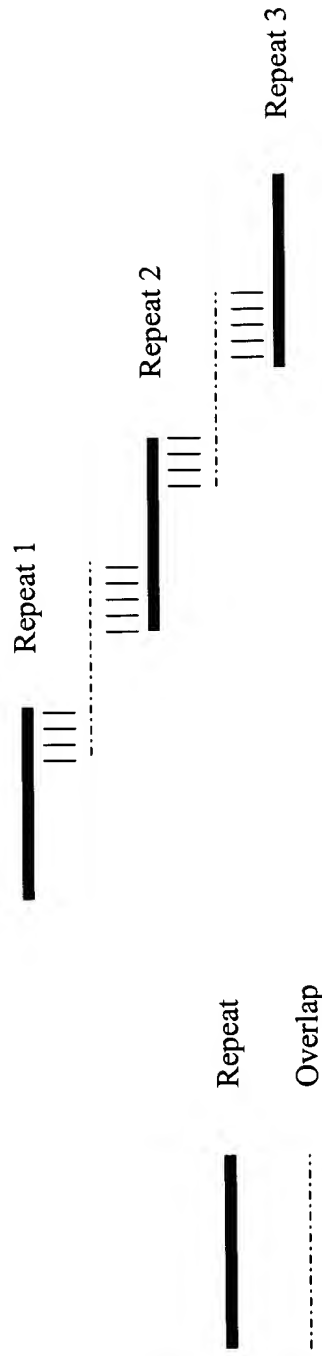
CA125



β -Tubulin

Figure 2

A Strategy for Placing Repeat Sequences in Contiguous Order Using Overlap Sequence Alignment



(SEQ ID NO: 158)	156
1 ATGPFVLPFTLNFTITNLQYEDMRHPGSRKFNTERVLOGLLLPFPKNTSVGPLYSGCRLLTLLRPEKDGAAATGVDAICTHRDPEDGLDRERLYWELSNLTNGIQELGPYTLDRNSLYVNGFTHRSSMPTTSTPGTSTVDVGTSGTSPSSPST	314
157 AAGPLLMPFTLNFTITNLQYEDMRHPGSRKFNTERVLOGLLLPFPKNTSVGPLYSGCRLLTLLRPEKDGAAATGVDAICTHRDPEDGLDRERLYWELSNLTNGIQELGPYTLDRNSLYVNGFTHRSSMPTTSTPGTSTVDVGTSGTSPSSPST	470
315 AAGPLLMPFTLNFTITNLQYEDMRHPGSRKFNTERVLOGLLLPFPKNTSVGPLYSGCRLLTLLRPEKDGAAATGVDAICTHRDPEDGLDRERLYWELSNLTNGIQELGPYTLDRNSLYVNGFTHRSSMPTTSTPGTSTVDVGTSGTSPSSPST	625
471 TAGPLLVPFTLNFTITNLQYEDMRHPGSRKFNTERVLOGLLLPFPKNTSVGPLYSGCRLLTLLRPEKDGAAATGVDAICTHRDPEDGLDRERLYWELSNLTNGIQELGPYTLDRNSLYVNGFTHRSSMPTTSTPGTSTVDVGTSGTSPSSPST	781
626 AAGPLLVPFTLNFTITNLQYEDMRHPGSRKFNTERVLOGLLLPFPKNTSVGPLYSGCRLLTLLRPEKDGAAATGVDAICTHRDPEDGLDRERLYWELSNLTNGIQELGPYTLDRNSLYVNGFTHRSSMPTTSTPGTSTVDVGTSGTSPSSPST	
(SEQ ID NO: 159)	156
1 SAGPLLVPFTLNFTITNLQYEDMRHPGSRKFNTERVLOGLLLPFPKNTSVGPLYSGCRLLTLLRPEKDGAAATGVDAICTHRDPEDGLDRERLYWELSNLTNGIQELGPYTLDRNSLYVNGFTHRSSMPTTSTPGTSTVDVGTSGTSPSSPST	312
157 TAGPLLVPFTLNFTITNLQYEDMRHPGSRKFNTERVLOGLLLPFPKNTSVGPLYSGCRLLTLLRPEKDGAAATGVDAICTHRDPEDGLDRERLYWELSNLTNGIQELGPYTLDRNSLYVNGFTHRSSMPTTSTPGTSTVDVGTSGTSPSSPST	468
313 TAGPLLVPFTLNFTITNLQYEDMRHPGSRKFNTERVLOGLLLPFPKNTSVGPLYSGCRLLTLLRPEKDGAAATGVDAICTHRDPEDGLDRERLYWELSNLTNGIQELGPYTLDRNSLYVNGFTHRSSMPTTSTPGTSTVDVGTSGTSPSSPST	624
469 EPGLLIPFTLNFTITNLQYEDMRHPGSRKFNTERVLOGLLLPFPKNTSVGPLYSGCRLLTLLRPEKDGAAATGVDAICTHRDPEDGLDRERLYWELSNLTNGIQELGPYTLDRNSLYVNGFTHRSSMPTTSTPGTSTVDVGTSGTSPSSPST	780
625 EPGLLIPFTLNFTITNLQYEDMRHPGSRKFNTERVLOGLLLPFPKNTSVGPLYSGCRLLTLLRPEKDGAAATGVDAICTHRDPEDGLDRERLYWELSNLTNGIQELGPYTLDRNSLYVNGFTHRSSMPTTSTPGTSTVDVGTSGTSPSSPST	
(SEQ ID NO: 160)	156
1 TAGPLLVPFTLNFTITNLQYEDMRHPGSRKFNTERVLOGLLLPFPKNTSVGPLYSGCRLLTLLRPEKDGAAATGVDAICTHRDPEDGLDRERLYWELSNLTNGIQELGPYTLDRNSLYVNGFTHRSSMPTTSTPGTSTVDVGTSGTSPSSPST	312
157 APVPLLIPFTLNFTITNLQYEDMRHPGSRKFNTERVLOGLLLPFPKNTSVGPLYSGCRLLTLLRPEKDGAAATGVDAICTHRDPEDGLDRERLYWELSNLTNGIQELGPYTLDRNSLYVNGFTHRSSMPTTSTPGTSTVDVGTSGTSPSSPST	468
313 APGPLLVPFTLNFTITNLQYEDMRHPGSRKFNTERVLOGLLLPFPKNTSVGPLYSGCRLLTLLRPEKDGAAATGVDAICTHRDPEDGLDRERLYWELSNLTNGIQELGPYTLDRNSLYVNGFTHRSSMPTTSTPGTSTVDVGTSGTSPSSPST	624
469 TASPPLLVPFTLNFTITNLQYEDMRHPGSRKFNTERVLOGLLLPFPKNTSVGPLYSGCRLLTLLRPEKDGAAATGVDAICTHRDPEDGLDRERLYWELSNLTNGIQELGPYTLDRNSLYVNGFTHRSSMPTTSTPGTSTVDVGTSGTSPSSPST	
(SEQ ID NO: 161)	156
1 ATGPVLLVPFTLNFTITNLQYEDMRHPGSRKFNTERVLOGLLLPFPKNTSVGPLYSGCRLLTLLRPEKDGAAATGVDAICTHRDPEDGLDRERLYWELSNLTNGIQELGPYTLDRNSLYVNGFTHRSSMPTTSTPGTSTVDVGTSGTSPSSPST	312
157 TASPPLLVPFTLNFTITNLQYEDMRHPGSRKFNTERVLOGLLLPFPKNTSVGPLYSGCRLLTLLRPEKDGAAATGVDAICTHRDPEDGLDRERLYWELSNLTNGIQELGPYTLDRNSLYVNGFTHRSSMPTTSTPGTSTVDVGTSGTSPSSPST	468
313 AASPPLLVPFTLNFTITNLQYEDMRHPGSRKFNTERVLOGLLLPFPKNTSVGPLYSGCRLLTLLRPEKDGAAATGVDAICTHRDPEDGLDRERLYWELSNLTNGIQELGPYTLDRNSLYVNGFTHRSSMPTTSTPGTSTVDVGTSGTSPSSPST	

Figure 3 (SEQ ID NOS: 158, 159, 160, and 161)

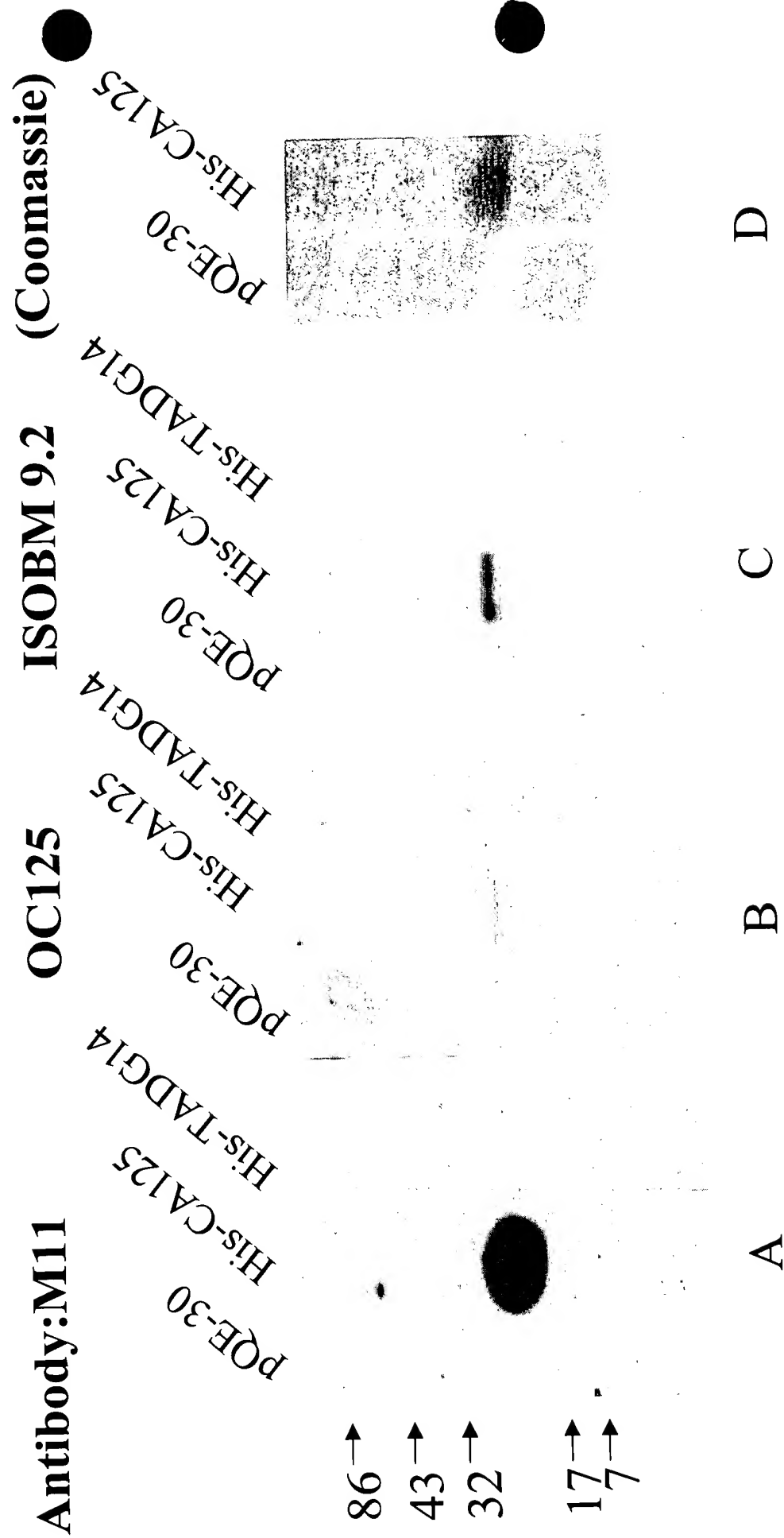
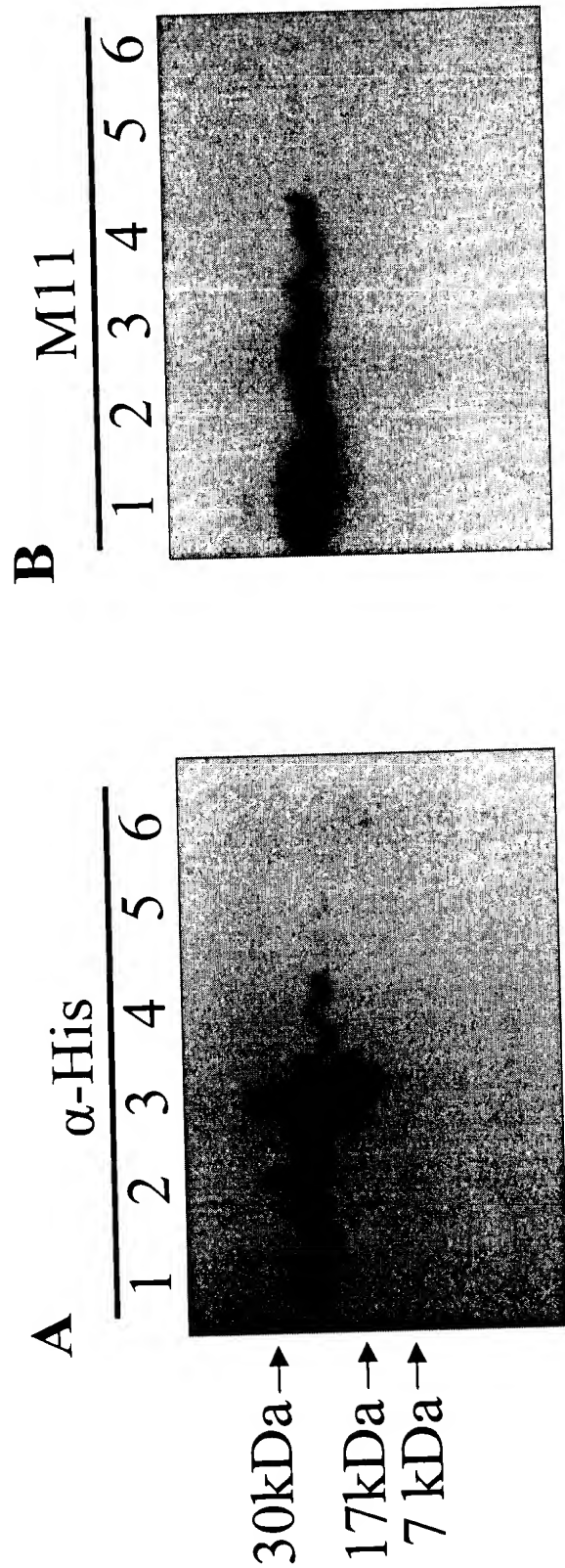
[illegible]

Figure 4

[illegible]

132203 8225360

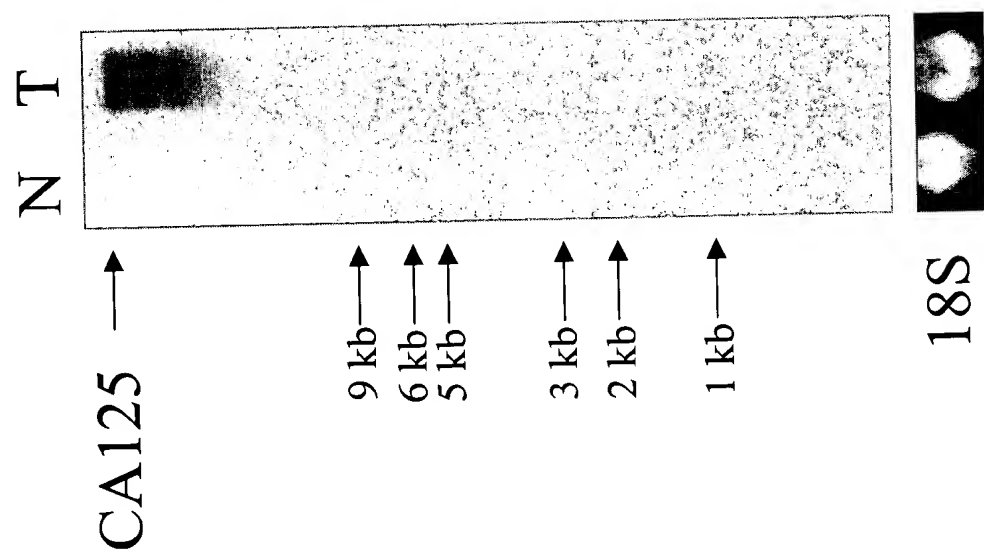


Figure 6

10/2000 86253650

Genomic Structure of a 156 Amino Acid Repeat Sequence of CA125

← ≈ 1900 bp →

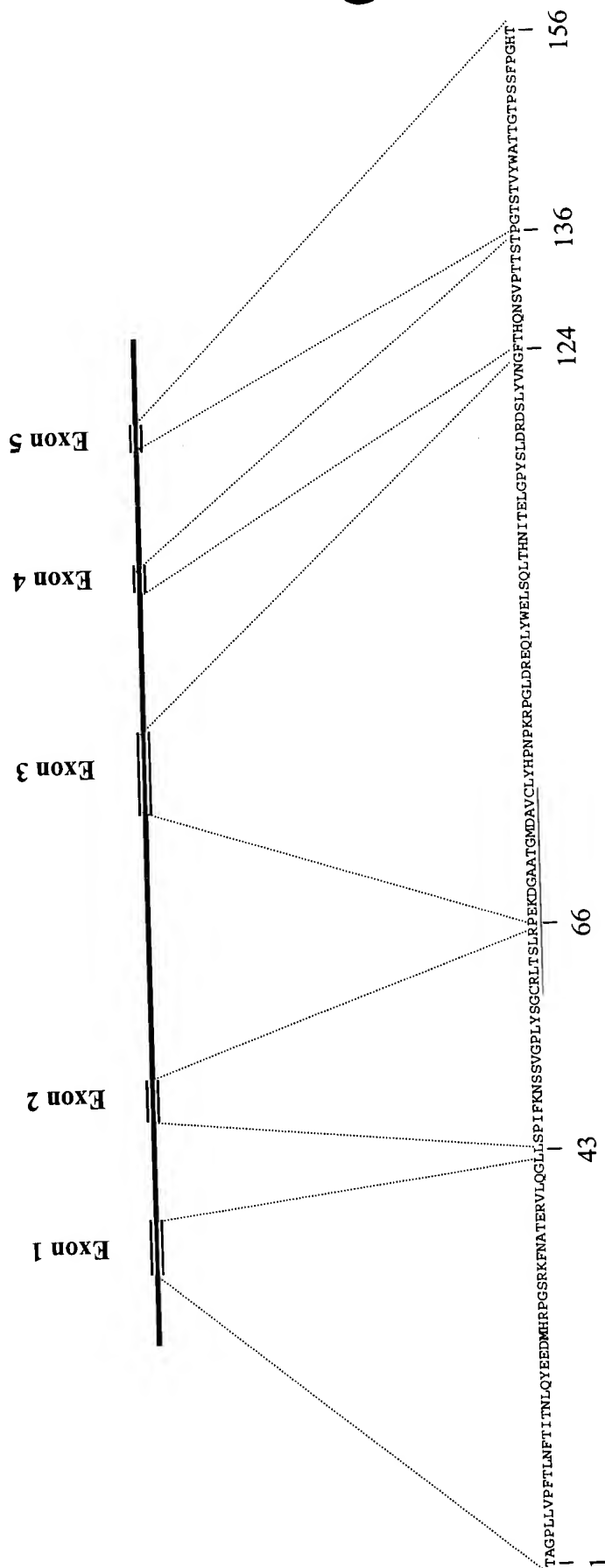


Figure 7B (SEQ ID NO: 163)

Exon 1

1

42

ATVPPFMPFTLNFTITNLQYEEDMRHPGSRKFNATERELQGL (SEQ ID NO: 164)
TAVPLLVPFTLNFTITNLQYGEDMRHPGSRKFNTTERVLQGL (SEQ ID NO: 165)
VPGPLLVPFTLNFTITNLQYEEAMRHPGSRKFNTTERVLQGL (SEQ ID NO: 166)
APGPLLVPFTLNFTITNLQYEEDMRHPGSRKFSTTERVLQGL (SEQ ID NO: 167)
APGPLLVPFTLNFTITNLQYEEDMRHPGSRKFNTTERVLQGL (SEQ ID NO: 168)
APGPLLVPFTLNFTITNLQYEVDMRHPGSRKFNTTERVLQGL (SEQ ID NO: 169)
SAGPLLVPFTLNFTITNLQYEEDMRHPGSRKFNTTERVLQGL (SEQ ID NO: 170)
AAGPLLMPFTLNFTITNLQYEEDMRRTGSRKFNTMESVLQGL (SEQ ID NO: 171)
TASPLLVLFTINCTITNLQYEEDMRRTGSRKFNTMESVLQGL (SEQ ID NO: 172)
AAGPLLVPFTLNFTITNLQYGEDMGHPGSRKFNTTERVLQGL (SEQ ID NO: 173)
TAGPLLIPFTLNFTITNLQYGEDMGHPGSRKFNTTERVLQGL (SEQ ID NO: 174)
TAGPLLVPFTLNFTITNLQYGEDMGHPGSRKFNTTERVLQGL (SEQ ID NO: 175)
TAGPLLVLFTLNFTITNLKYEEDMHRPGSRKFNTTERVLQTL (SEQ ID NO: 176)
TAGPLLVPFTLNFTITNLQYEEDMHRPGSRKFNTATERVLQGL (SEQ ID NO: 177)
TAGPLLVPFTLNFTITNLQYEEDMHRPGSRKFNTTERVLQGL (SEQ ID NO: 178)
TAGPLLVPFTLNFTITNLQYEEDMHRPGSRKFNTTERVLQGL (SEQ ID NO: 179)
APVPLLIPTLNFTITNLQYEEDMHRPGSRKFNTTERVLQGL (SEQ ID NO: 180)
ATGPVLLPFTLNFTITNLQYEEDMHRPGSRKFNTTERVLQGL (SEQ ID NO: 181)
AAGPLLVPFTLNFTITNLQYEEDMHHPGSRKFNTTERVLQGL (SEQ ID NO: 182)
SAGPLLVPFTLNFTITNLQYEEDMHHPGSRKFNTTERVLQGL (SEQ ID NO: 183)
TASPLLVLFTINFTITNQRYEENMHHPGSRKFNTTERVLQGL (SEQ ID NO: 184)
TASPLLVLFTINFTITNLRYEENMHHPGSRKFNTTERVLQGL (SEQ ID NO: 185)
EPGPLLIPFTNFNTITNLHYEENMQHPGSRKFNTTERVLQGL (SEQ ID NO: 186)
EPGPLLIPFTNFNTITNLRYEENMQHPGSRKFNTTERVLQGL (SEQ ID NO: 187)
APVPLLIPTLNFTITNLHYEENMQHPGSRKFNTTERVLQGL (SEQ ID NO: 188)
APVPLLIPTLNFTITDLHYEENMQHPGSRKFNTTERVLQGL (SEQ ID NO: 189)
AASPLLVLFTLNFTITNLRYEENMQHPGSRKFNTTERVLQGL (SEQ ID NO: 190)
TAGPLLVPFTLNFTITNLKYEEDMHCPSGRKFNTTERVLQSL (SEQ ID NO: 191)
AASHLLILFTLNFTITNLRYEENMW.PGSRKFNTTERVLQGL (SEQ ID NO: 192)
TGVVSEEPFTLNFTINNLRYMADMGQPGSLKFNITDNVMKHL (SEQ ID NO: 193)
AMGYHLKTLTINFTISNLQYSPDMGKSATFNSTEGVLQHLL (SEQ ID NO: 194)

0005730-000701

Figure 7C

43

65

LKPLFRNSSLEYLYSGCRLASLR	(SEQ ID NO: 195)
LKPLFKNTSVSSLYSGCRLTLLR	(SEQ ID NO: 196)
LKPLFKNTSVGPLYSGCRLTLLR	(SEQ ID NO: 197)
LKPLFKSTSVGPLYSGCRLTLLR	(SEQ ID NO: 198)
LKPLFKSTSVGPLYSSCRLTLLR	(SEQ ID NO: 199)
LKPLFKNTSVGPLYSGCRLTSLR	(SEQ ID NO: 200)
LGPIFKNTSVGPLYSGCRLTSLR	(SEQ ID NO: 201)
LGPMFKNTSVGLLYSGCRLTLLR	(SEQ ID NO: 202)
LGPMFKNTSVGPLYSGCRLTLLR	(SEQ ID NO: 203)
LGPMFKNTSVGPLYSGCRLTSLR	(SEQ ID NO: 204)
LGPLFKNSSVGPLYSGCRLISLR	(SEQ ID NO: 205)
LGPLFKNSSVDPLYSGCRLTSLR	(SEQ ID NO: 206)
LSPIFKNSSVGPLYSGCRLTSLR	(SEQ ID NO: 207)
LSPIFKNTSVGPLYSGCRLTLLR	(SEQ ID NO: 208)
LSPLFQRSSLGARYTGCRVIALR	(SEQ ID NO: 209)
LRPLFKNTSVSSLYSGCRLTLLR	(SEQ ID NO: 210)
LRPLFKNTSVGPLYSGSRLTLLR	(SEQ ID NO: 211)
LRPLFKNTSIGPLYSSCRLTLLR	(SEQ ID NO: 212)
LRPLFKSTSVGPLYSGCRLTLLR	(SEQ ID NO: 213)
LRPVFKNTSVGLLYSGCRLTLLR	(SEQ ID NO: 214)
LRPVFKNTSVGPLYSGCRLTLLR	(SEQ ID NO: 215)
LRSLFKSTSVGPLYSGCRLTLLR	(SEQ ID NO: 216)
LRSLFKSTSVGPLYSGCRLTSLR	(SEQ ID NO: 217)
LTPLFKNTSVGPLYSGCRLTLLR	(SEQ ID NO: 218)
LTPLFRNTSVSSLYSGCRLTLLR	(SEQ ID NO: 219)
LMPLFKNTSVSSLYSGCRLTLLR	(SEQ ID NO: 220)
RPLFQKSSM.GPFYLGCLISLR	(SEQ ID NO: 221)

SECRET

Figure 7C

Exon 3

66

123

PEKDSSAMAVDAICTHRPDPEDLGLDRERLYWELSNLTNGIQELGPYTLDRNSLYVNG (SEQ ID NO: 222)
PEKDGAATGVDAICTHRLDPKSPGLNREQLYWELSKLTNDIEELGPYTLDRNSLYVNG (SEQ ID NO: 223)
PKKDGAATGVDAICTHRLDPKSPGLNREQLYWELSKLTNDIEELGPYTLDRNSLYVNG (SEQ ID NO: 224)
PEKDGTATGVDAICTHHPDPKSPRLDREQLYWELSQLTHNITELGHYALDNDSLFVNG (SEQ ID NO: 225)
PEKDGEATGVDAICTHRPDPGTGPGLDREQLYLELSQLTHSITELGPYTLDRDSLYVNG (SEQ ID NO: 226)
PEKDGAATGMDAVCLYHPNPKRPGLDREQLYWELSQLTHNITELGPYSLDRDSLYVNG (SEQ ID NO: 227)
PEKDGAATGMDAVCLYHPNPKRPGLDREQLYCELSQLTHNITELGPYSLDRDSLYVNG (SEQ ID NO: 228)
PEKDGAATRVDAACTYRDPKSPGLDREQLYWELSQLTHSITELGPYTLDRVSLYVNG (SEQ ID NO: 229)
PKKDGAATKVDAICTYRDPKSPGLDREQLYWELSQLTHSITELGPYTQDRDSLYVNG (SEQ ID NO: 230)
PKKDGAATKVDAICTYRDPKSPGLDREQLYWELSQLTHSITELGPYTQDRDSLYVNG (SEQ ID NO: 231)
PEKDGAATRVDAVCTHRPDPKSPGLDRERLYWKLSQLTHGITELGPYTLDRHSLYVNG (SEQ ID NO: 232)
PEKDGVAATRVDAICTHRPDPKIPGLDRQQLYWELSQLTHSITELGPYTLDRDSLYVNG (SEQ ID NO: 233)
SEKDGAATGVDAICIHHLDPKSPGLNRERLYWELSQLTNGIKELGPYTLDRNSLYVNG (SEQ ID NO: 234)
SEKDGAATGVDAICTHRLDPKSPGLDREQLYWELSQLTNGIKELGPYTLDRNSLYVNG (SEQ ID NO: 235)
SEKDGAATGVDAICTHRLDPKSPGVDRREQLYWELSQLTNGIKELGPYTLDRNSLYVNG (SEQ ID NO: 236)
SEKDGAATGVDAICTHRVDPKSPGVDRREQLYWELSQLTNGIKELGPYTLDRNSLYVNG (SEQ ID NO: 237)
SEKDGAATGVDAICTHHLNPQSPGLDREQLYWQLSQMTNGIKELGPYTLDRNSLYVNG (SEQ ID NO: 238)
PEKRGAAATGVDITICTHRLDPLNPGLDREQLYWELSKLTRGIIELGPYLLDRGSLYVNG (SEQ ID NO: 239)
PEKNGAATGMDAICSHRLDPKSPGLNREQLYWELSQLTHGIKELGPYTLDRNSLYVNG (SEQ ID NO: 240)
PEKNGAATGMDAICSHRLDPKSPGLDREQLYWELSQLTHGIKELGPYTLDRNSLYVNG (SEQ ID NO: 241)
PEKHGAATGVDAICTLRLDPTGPGLDREQLYWELSQLTNSVTELGPYTLDRDSLYVNG (SEQ ID NO: 242)
PEKHGAATGVDAICTLRLDPTGPGLDREQLYWELSQLTNSITELGPYTLDRDSLYVNG (SEQ ID NO: 243)
PEKHEAATGVDITICTHRVDPGPGLDREQLYWELSQLTNSITELGPYTLDRDSLYVNG (SEQ ID NO: 244)
PEKQEAATGVDITICTHRVDPGPGLDREQLYWELSQLTNSITELGPYTLDRDSLYVNG (SEQ ID NO: 245)
PEKQEAATGVDITICTHRVDPGPGLDREQLYWELSQLTNSITELGPYTLDRDSLYVDG (SEQ ID NO: 246)
PEKDKAATRVDAICTHHPDPQSPGLNREQLYWELSQLTHGITELGPYTLDRDSLYVDG (SEQ ID NO: 247)
SVKNGAETRVDLLCTYLQPLSGPGLPIKQVFHELSQQTHGITRLGPYSLDKDSLYLNG (SEQ ID NO: 248)
PEKDGAATGVDTTCTYHPDPVGPGLDIQQLYWELSQLTHGVTQLGFYVLDLDRDSLFING (SEQ ID NO: 249)

Figure 7C

Exon 4

124 135
 FTHRSMPTTST (SEQ ID NO: 250)
 FTHRSMPTTSI (SEQ ID NO: 251)
 FTHRTSVPTTST (SEQ ID NO: 252)
 FTHRTSVPTTST (SEQ ID NO: 253)
 FTHRSSVPTTSS (SEQ ID NO: 254)
 FTHRSSVPTTST (SEQ ID NO: 255)
 FTHRSSVAPTST (SEQ ID NO: 256)
 FTHRSSGLTTST (SEQ ID NO: 257)
 FTHRSGFGLTTST (SEQ ID NO: 258)
 FTHRSSFLTTST (SEQ ID NO: 259)
 FTHRNFPITST (SEQ ID NO: 260)
 FTHRSSVPTTSI (SEQ ID NO: 261)
 FTHQSSVPTTST (SEQ ID NO: 262)
 FTHQTSAPNTST (SEQ ID NO: 263)
 FTHQTFAPNTST (SEQ ID NO: 264)
 FTHQNSVPTTST (SEQ ID NO: 265)
 FTHQSSMTTTRT (SEQ ID NO: 266)
 FTHWIPVPTTST (SEQ ID NO: 267)
 FTHWSPIPTTST (SEQ ID NO: 268)
 FTHWSSGLTTST (SEQ ID NO: 269)
 FHPRSSVPTTST (SEQ ID NO: 270)
 FNPVSSVPTTST (SEQ ID NO: 271)
 FNPWSSVPTTST (SEQ ID NO: 272)
 FTQRSSVPTTSI (SEQ ID NO: 273)
 FTQRSSVPTTST (SEQ ID NO: 274)
 FTQRSSVPTTSV (SEQ ID NO: 275)
 YNEPGLDEPPTT (SEQ ID NO: 276)
 YAPQNLIRGEY (SEQ ID NO: 277)

Exon 5

136 156
 PGTSTVDVGTSGTPSSSPSPT (SEQ ID NO: 278)
 PGTSTVDLRTSGTPSSLSSPTIM (SEQ ID NO: 279)
 PGTSTVDLGTSGTPFSLPSPA (SEQ ID NO: 280)
 PGTSTVDLG.SGTPSSLPSPT (SEQ ID NO: 281)
 PGTSTVDLG.SGTPSLPSPT (SEQ ID NO: 282)
 PGTSTVDLGTSGTPSSLPSPT (SEQ ID NO: 283)
 PGTPTVDLGTSGTPVSKPGPS (SEQ ID NO: 284)
 PWTSTVDLGTSGTPSPVPSPT (SEQ ID NO: 285)
 PGTSTVYWATTGTPSSFPGHT (SEQ ID NO: 286)
 PGTSTVHLATSGTPSSLPGHT (SEQ ID NO: 287)
 PGTSTVHLATSGTPSPLPGHT (SEQ ID NO: 288)
 PDTSTMHLATSRTPASLSGPT (SEQ ID NO: 289)
 PGTSVHLETSGTPASLPGHT (SEQ ID NO: 290)
 PGTSVHLETTGTPSSFPGHT (SEQ ID NO: 291)
 PGTSTVHLGTSETPSSLPRPI (SEQ ID NO: 292)
 PGTSIVNLGTSGIPPSLPETT (SEQ ID NO: 293)
 PGTFTVQPETSETPSSLPGPT (SEQ ID NO: 294)
 PGTPTVDLGTSGTPVSKPGPS (SEQ ID NO: 295)
 PGTPTVYLGASKTPASIFGPS (SEQ ID NO: 296)
 PKPATTFLLPPLSEATT..... (SEQ ID NO: 297)
 QINFHIVNWNLSNPDPTSSEY (SEQ ID NO: 298)

Figure 7C

13250 bp

Structure of Amino Terminal Domain

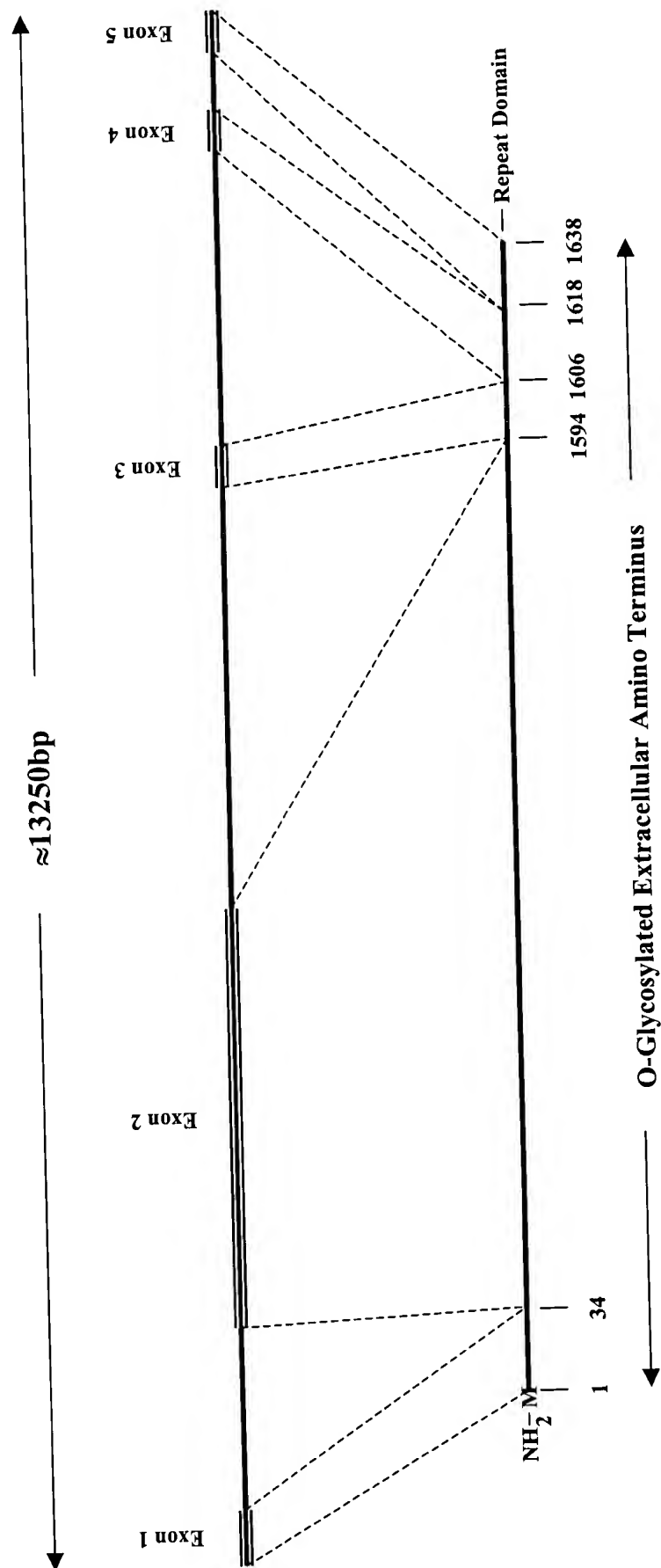


Figure 8A

1	MEHITKIPNE	AAHRTGIRPV	KGPQTSTSPA	SPKGLHTGGT	KRMETITIAL	901	ISATFPVPE	SPHESEATAS	WVTHPAVIST	WVPRTPPNYS	HSEPDTPPSI
51	KTITLTKTT	SRATLTTSVY	TPILGLTLP	NASRQMASTI	LTEMMITTPY	951	ATSPGAETS	DFPTITVSPD	VPDMVTSQVT	SSGTDTSITI	PILLSSGEP
101	VFPDVPETTS	SLATSLGAET	STALPRITPS	VLNRESETTA	SLVSRSGAER	1001	ETTSFITYS	ETHTSSAIP	LPVSPGASKM	LTSLVISSGT	DSTTFFTLT
151	SPVIQTLDVS	SSEPDTIASW	VIHPAETIPT	VSKTTPNFFH	SELDTVSSTA	1051	ETPYEPETTA	IQLIHPAETN	TMVPRITPKF	SHSKSDTTL	VAITSPGPEA
201	TSHGADVSSA	IPTNISPSEL	DALTPLVIS	GTDTSTTFPT	LTKSPHETET	1101	SSAVSTTIS	PMSDLVTSL	VPSSGIDTST	TFPILSETPY	EPETTA
251	RTTWLTHPAE	TSSITRTIP	NFSHESDAT	PSLATSPGAE	TSSAIPIMTV	1151	HPAETSTVS	GTIPNFSHRG	SDTAPSMVTS	PGVDRSGVP	TTTIPPSLPG
301	SPGAEDLVTS	QVTSSGTRN	MTIPTLTSP	GEPKTIASLV	THPEAQTS	1201	VVTSQVTS	TDSTAIPTL	TPSPGEPEIT	ASSATHPGTG	TGFTVPIRTV
351	IPTSTISPAV	SRLVTSMTS	LAAKTSTNR	ALTNSPGEP	TTVSLVTHPA	1251	PSSEPDTMAS	WVTHPPQIST	PVSRITSSFS	HSSPDATPVM	ATSPRTEASS
401	QTSPIVPWTT	SIFFHKSDDT	TPSMTTSHGA	ESSAVPTPT	VSTEVPGVVT	1301	AVLTTSIPGA	PEMVTQITS	SGAATSTTVP	TLTHSPGMPE	TTALLSIHPR
451	PLVTSSRAVI	STTIPILT	PGEPTTPSM	ATSHGEEASS	AIPTPTVSPG	1351	TETSKTFPAS	TVFPQVSEIT	ASLTIRPGAE	TSTALPTQTT	SSLFTLLVTG
501	VPGVVTSLVT	SSRAVTSTTI	PILTFSLGEP	ETTPSMATSH	GTEAGSAVPT	1401	TSRVDLSPIA	SPGVSAKTAP	LSTHPGTETS	TMIPISILSL	GLLETTGLLA
551	VLPEVPGMVT	SLVASSRAVT	STTLPTLTLS	PGEPTTPSM	ATSHGAEASS	1451	TSSSAETSTS	TLTLTVSPAV	SGLSASAIT	DKPQIVTSWN	TETSPSVTSV
601	TVPTVSPEVP	GVVTSLVTS	SGVNSTSIPT	LILSPGELET	TPSMAISHGA	1501	GPPEFSRTVT	GTMTLIPSE	MPTPPKTSHG	EGVSPTTILR	TTMVEATNLA
651	EASSAVPTPT	VSPGVSGVVT	PLVTSSRAVT	STTIPILT	SSPEPTPSM	1551	TTGSSPTVAK	TTTTFNTLAG	SLFTPLTTPG	MSTLASESVT	SRTSYNHRSW
701	ATSHGVEASS	AVLTVSPEVP	GMVTSLVTS	RAVTSSTIPT	LTISSDEPET	1601	ISTTSSYNRR	YWTPATSTPV	TSTFSPGIST	SSIPSSAAT	VPFMVFFTLN
751	TTSLVTHSEA	KMISAIPILA	VSPTVQGLVT	SLVTSSGSET	SAFSLTVAS	1651	FTITNLQVEE	DMRHGSRKF	NATERELQGL	LKPLFRNSSL	EYLYSGCRLA
801	SQPETIDSWV	AHPGTEASSV	VPILTAVSTGE	PFTNISLVTH	PAESSSTLPR	1701	SLRPEKDSSA	MAVDAICTHR	PDPEDLGLDR	ERLYWELSNL	TNGIQE
851	TTSRFSHSEL	DTMPSTVISP	EAESSAIST	TISPGIPGVL	TSLVTSSGRD	1751	TLDRNSLYVN	GFTHRSSMPT	TSTPGTSTVD	VGTSGLPSSS	PSPT

Figure 8B (SEQ ID NO: 299)

Structure of Carboxy Terminal Domain

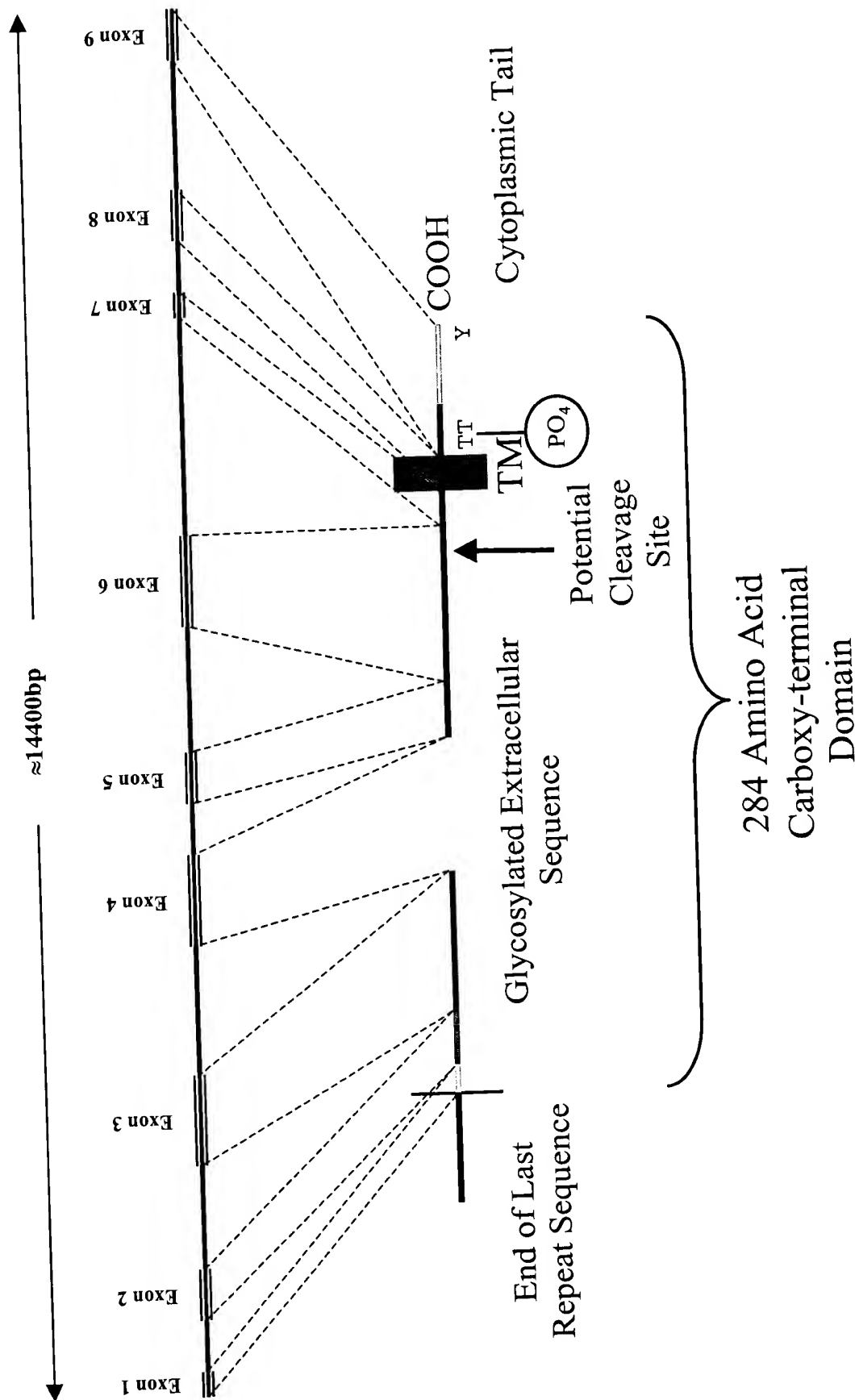


Figure 9A

734363" 86233660

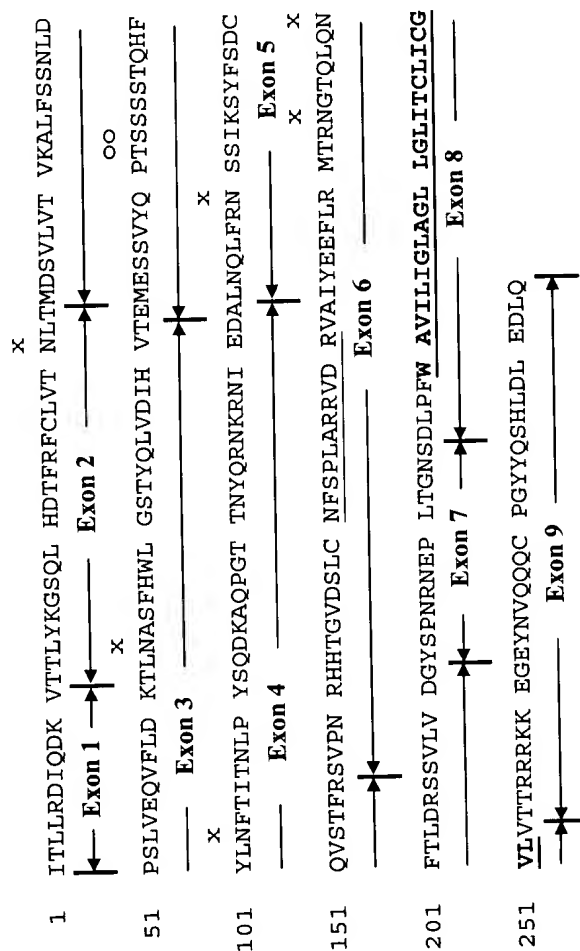


Figure 9B (SEQ ID NO: 300)

Proposed Structure of CA125

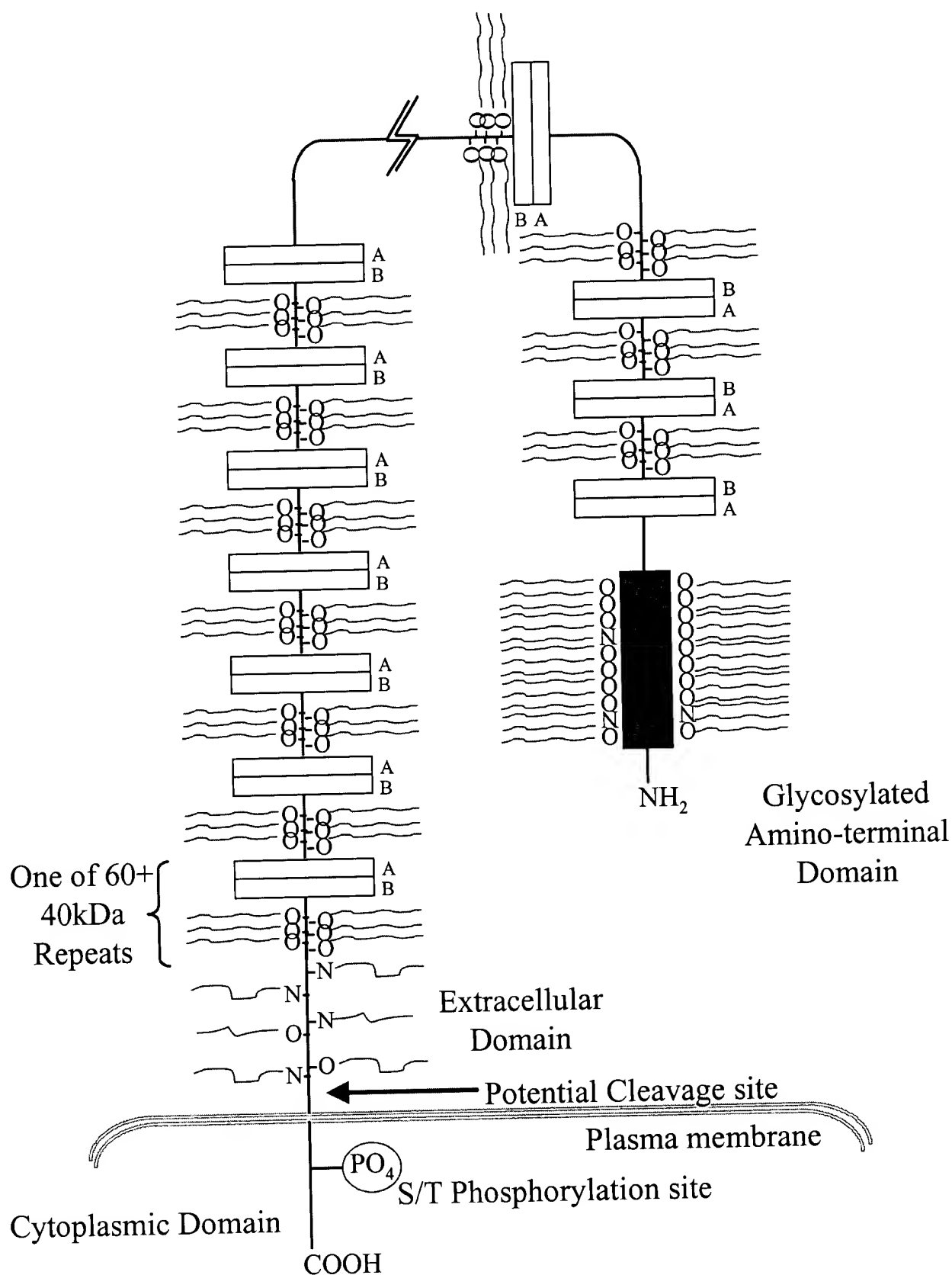


Figure 10